

Resource Summary Report

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Max Planck Institute of Biochemistry NGS Core Facility

RRID:SCR_025746

Type: Tool

Proper Citation

Max Planck Institute of Biochemistry NGS Core Facility (RRID:SCR_025746)

Resource Information

URL: <https://www.biochem.mpg.de/ngs>

Proper Citation: Max Planck Institute of Biochemistry NGS Core Facility (RRID:SCR_025746)

Description: Facility for high-throughput sequencing. Provides Next-Generation Sequencing services, supports library preparation and quality control for various applications including RNA-Seq: rRNA depletion-total RNA, mRNAseq; DNA-Seq: ChIP-Seq, Cut andTag seq, Hi-Cseq, Micro-Cseq, WGS; Single Cell: scRNAseq, scATACseq, snRNAseq, seRNAseq.

Abbreviations: MPIB-NGS

Synonyms: NGS Core Facility, Max Planck Institute of Biochemistry NGS Core Facility

Resource Type: access service resource, core facility, service resource

Keywords: Next-Generation Sequencing services, high-throughput sequencing, library preparation, quality control

Availability: Restricted

Resource Name: Max Planck Institute of Biochemistry NGS Core Facility

Resource ID: SCR_025746

Record Creation Time: 20240918T053245+0000

Record Last Update: 20260912T200451+0000

Ratings and Alerts

No rating or validation information has been found for Max Planck Institute of Biochemistry NGS Core Facility.

No alerts have been found for Max Planck Institute of Biochemistry NGS Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Bonnet J, et al. (2026) Histone modification cross-talk and protein complex diversification confer plasticity to Polycomb repression. *Genes & development*, 40(1-2), 43.

Kobayashi W, et al. (2026) Protocol for integrative analysis of transcription factor-nucleosome interactions using SeEN-seq and cryo-EM structure determination. *STAR protocols*, 7(1), 104295.

Li R, et al. (2026) Single-molecule dynamics of the TRiC chaperonin system in vivo. *Nature*, 652(8109), 481.

Kobayashi W, et al. (2026) Feed-forward loops by NR5A2 ensure robust gene activation during pre-implantation development. *Development (Cambridge, England)*, 153(1).

Andree GA, et al. (2026) Cysteine availability tunes ubiquitin signaling via inverse stability of LRR58 E3 ligase and its substrate CDO1. *Nature communications*, 17(1).

Guyot C, et al. (2026) IL4i1 activity generates oncometabolites that rescue neuroblastoma cells from oxidative death. *Cell reports*, 45(6), 117441.

Deiser AM, et al. (2026) A role for nucleosome remodellers during resection of deprotected telomeres in yeast. *PloS one*, 21(7), e0352656.

Kang M, et al. (2025) Single-cell metabolome and RNA-seq multiplexing on single plant cells. *Proceedings of the National Academy of Sciences of the United States of America*, 122(43), e2512828122.

Rodschinka G, et al. (2025) Comparative CRISPRi screens reveal a human stem cell dependence on mRNA translation-coupled quality control. *Nature structural & molecular biology*, 32(10), 1932.

Hermann MD, et al. (2025) Normal macrophage signaling and gene expression in Rosa26 Cas9-expressing mice. *ImmunoHorizons*, 9(11).

Russier M, et al. (2025) Differential cell survival outcomes in response to diverse amino acid stress. *Life science alliance*, 8(11).

Bright AR, et al. (2025) Temporal control of progenitor competence shapes maturation in GABAergic neuron development in mice. *Nature neuroscience*, 28(8), 1663.

Kobayashi W, et al. (2025) CUT&Tag for Transcription Factor Binding Profiles During Mammalian Zygotic Genome Activation. *Methods in molecular biology* (Clifton, N.J.), 2923, 77.

Iermak I, et al. (2025) Molecular mechanisms governing the formation of distinct Upf1-containing complexes in yeast. *Cell reports*, 44(10), 116415.